## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

## **Listing Of Claims**

- 1. (Currently amended) A composition comprising a protein in crystalline form, wherein at least a portion of the protein has at least 90% identity with residues 51-778 of SEQ. ID No. 1 consists of SEQ. ID No. 3.
- 2-3. (Cancelled)
- 4. (Currently amended) A composition according to claim 1 wherein the protein <u>crystal</u> diffracts X-rays for a determination of structure coordinates to a resolution <u>greater less</u> than 3.0 Angstroms.
- 5. (Original) A composition according to claim 1 wherein the protein crystal has a crystal lattice in a P2<sub>1</sub> space group.
- 6. (Original) A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å,  $\alpha=\gamma=90^{\circ}$ ,  $\beta=114.6^{\circ}$ .
- 7. (Currently amended) A method for forming a crystal of a protein comprising:

  forming a crystallization volume comprising[:] a precipitant solution and a protein

  wherein at least a portion of the protein has at least 90% identity with residues 51 778 of

SEQ. ID No. 1 that consists of SEQ. ID No. 3; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

8. (Currently amended) A method according to claim 7 wherein at least a portion of the protein has at least 95% identity with residues 51 778 of SEQ. ID No. 1 is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

## 9. (Cancelled)

- 10. (Currently amended) A method according to claim 7 wherein the protein <u>crystal</u> diffracts X-rays for a determination of structure coordinates to a resolution <u>greater\_less</u> than 3.0 Angstroms.
- 11. (Original) A method according to claim 7 wherein the protein crystal has a crystal lattice in a P21 space group.
- 12. (Original) A method according to claim 7 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å,  $\alpha = \gamma = 90^{\circ}$ ,  $\beta = 114.6^{\circ}$ .
- 13. (Original) A method according to claim 7, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.
- 14. (Cancelled)
- 15. (Currently amended) A composition according to claim 14 16 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.
- 16. (Currently amended) A composition comprising an isolated a protein consisting of SEQ. ID No. 3.

17. (Currently amended) A method of identifying an entity that associates with a protein, comprising:

taking structure coordinates from diffraction data obtained from a <u>protein\_crystal</u> formed according to the method of claim 7; has at least 90% identity with SEQ. ID No. 3; and performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

- 18. (Currently amended) A method according to claim 17 wherein the protein <u>from</u> which the protein crystal is formed has at least 95% identity with SEQ. ID No. 3. is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.
- 19. (Original) A method according to claim 17 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å,  $\alpha = \gamma = 90^{\circ}$ ,  $\beta = 114.6^{\circ}$ .
- 20. (Original) A method according to claim 17, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.
- 21. (Original) A method according to claim 17, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

22-23. (Cancelled)